

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANTS: Mark L. Gonzalgo and Peter A. Jones

(ii) TITLE OF INVENTION: A CANCER DIAGNOSTIC METHOD BASED UPON  
DNA METHYLATION DIFFERENCES

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIS WRIGHT TREMAINE  
(B) STREET: 2600 Century Square, 1501 Fourth Avenue  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: U.S.A.  
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: PC compatible  
(C) OPERATING SYSTEM: Windows95  
(D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: to be assigned  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Oster, Jeffrey B.  
(B) REGISTRATION NUMBER: 32,585  
(C) REFERENCE/DOCKET NUMBER: 47675-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206 628 7711  
(B) TELEFAX: 206 628 7699

### (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: GaL1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

1 CCCGCGACCT AAGCCAGCGA CTTACCACGT TAGTCAGCTA AGAAGTGGCA 50

51 GAGCTGGGAT TCGAACCTAT AAAGAACTCT GAAGCCTGGG TATTTTACATA 100  
 101 TGACACTTTA CATAATGCGC CACGGGGTAG TCGGAGGGGG AGGTCCATCT 150  
 151 CCCTTTCCCT TGCTGTCCAT CTCCACAGAA AAGAAGCAAG TGGAGGACAG 200  
 201 GAGCCAGAAA GTCATCTGGC CGCGGATCAT TCCGGAGTGA CCCCCGCCGC 250  
 5 251 CACCACTCGC ATAGTCCGCT TATGGCGGGA GGGCACCTCA GAGATTCTCA 300  
 301 CAGGGGCTGT GCGGCCAGAA CCAGAAGTGC AAAGCACCGT TAGCGACTCT 350  
 351 ATCGCCCCCT GCCGCCTGTG GCGCCCAGTC CGAAGCTGCT GTTTTCAGGA 400  
 401 GGGCTAGTGG GCTAAGAAAA GAGCTCACCG ACTGACTGCC CAACAGCTGT 450  
 451 TGCGAGCCAG TGCTAGGCTG CAGACAGCCT TGCCAAATGT GGTGACATAA 500  
 10 501 GCGGGAGGGG GGAACATTTA GAGAGCCCTA 530

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: GaL2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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1 CTAGGGTAGG CTGGTCTGTG CTGGATACGC GTGTTCTTCT GCGGAGTTAA 50  
 51 AGGGTCGGGG ACGGGGGTTC TGGACTTACC AGAGCAATTC CAGCCGGTGG 100  
 101 GCGTTTGACA GCCACTTAAG GAGGTAGGGA AAGCGAGCTT CACCGGGCGG 150  
 151 GCTACGATGA GTAGCATGAC GGGCAGCAGC AGCAGCAGCC AGCAAAAGCC 200  
 201 TAGCAAAGTG TCCAGCTGCT GCACTGCCGC GGGGACTCCC ACATCACCAT 250  
 30 251 GACTAGTTGT GCAACTCTGC AGCAGAAACG GCTTCCGAGG AACACAGGAT 300  
 301 CGCGGGGG 308

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: GaL4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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1 GCTTCCTTTT TCTCGGCTTT CCTCACTATC CTCTCCCTGT TCGAGAGTAT 50  
 51 CTCCACCAGC ACCGAGCCTC ACACGGGCTG TGCCTCCATC TTTGGAATGC 100  
 101 CTACCCTTCT TTCTTGCGAA GCCCCTCCCA GGGCCAGCCC TTGTGCACCG 150  
 50 151 GCTCAAGGGG ACTGCTCTCC TGCCTCG 177

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148  
(B) TYPE: oligonucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HuN1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
1 TTGCGCCGAT CGTCAAGAAC CTCTCATCCC TGGCAGCAGC AAAGCCAATA 50
51 TATTTCATT TCTTATTTC GTTTGCCACC AAAACAAAGC TGC GCGCGGC 100
101 TGAGGGCAGG AAGGCGCTGA GACCGACCGA GAAGAAGGGA CGTCCCGG 148
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 384  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HuN2 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
1 CAGGCCCCGCC GAGACTCCAC TCCA ACTACC AGGAAATTTTC CCGTGGAGCT 50
51 TCAATTCCTG GGACCCTCCT ACTGCGGGGA GAGTGGTTTC CCTGCCCCAC 100
101 ACCATGCCCT AGGCCCCGAGT CTGCGGCTCT TGGGGGATCT CTCCGAGCTC 150
151 CGACACCGTG TTCGGACCGG GTGCGCCCTG CCGCTGGGGC TCAAGCCTGC 200
201 AGGCGTGAGA ACCGGGGGAC TCTCTATGGC ACCAAGAGCT TCACCGTGAG 250
251 CGTAGGCAGA AGCTTCGCTT TGATCCTAGG GCTTACAAAG TCCTCCTTTG 300
301 GCTGCCCATG ATGGTAAAAG GGCAGTTGCT CACAAAGCGC GAGTGTGTGT 350
351 GCCAGACAGT GTAAATGAGT GTTGGGACCG GCGT 384
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HuN3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
1 GGGTCCGTTT GTGAATGCAT GAGCAGGGTG TGAGCGCCAG GGGGTTACAC 50
51 TTCTCACGGG TTA AAACCCA GACAACTTCA CGAGGGAACC ACGTGCCATT 100
101 TTAACAGCGT ACGGTCGGGA TCGTGGGACG TCATTAAACG GAGTGGGTTG 150
151 AGTATGTGAC TCTGTCACCC ATTTTCTG
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HuN4 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
1  CCCCCGCGGG CAGAATCCAA GTGAGTCAGA CACATTGCTC CCTCCCTGCT 50
51 GCTGCCAGTC CATCTCTTTG CCAACAAACC TGCTTAAAAT GCCAAAGCTG 100
101 GTCCAAAGTT TCAGGAAAAC AACTTCCGCC AGAGGGCACG TAGAGGGCAC 150
151 AGATGCTATA GATGCTTCTC TGACAAACAC TCCTGACCCC CTTGACAGAT 200
201 TGGAAAATAC ATGGTTCAGA AAGGGTGAGA GATTTCAACT TGAGAAAGTGA 250
251 AACTAGGAAA AGATGGAAGG TGTCCGGATT TCTAGCTCAA GTCCACACAC 300
301 TGCTTCTGCT GCGGTGACTA AATCGTGGCT GTGTTCTCAT CACCTGCCTC 350
351 GCGGCGCGC 359
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HuN5 primer

```
1  GGCGGGCCTG GGCACCGCGG AGGGGGGGCT TTTCTGCGCC CGGCGAAGCG 50
51 TGGAAGTTGC GCCCTGAGGC AGCGCGGCGA GACCAGTCCA GAGACCGGGG 100
101 CGAGCCTCCT CAGGATTCTT CGCCCCAGTG CAGATGCTGT GAGCTTAGAC 150
151 GAGGACAGGG CATGGCACTC GGCTTGGCCC GTAGTGGACG GTGTTTTTGC 200
201 AGTCATGAAC CCAAACGCCG CAAACCTTGA CCGTTTCCCC ACCCGTGTGT T 251
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HuN6 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
1  TGAGAGCAGC ATCCTCCCCT GCGTGTGGTT CTCTAACTTA CCTCCTGTAT 50
51 GGGGTCTGCG GACCCAGCAC ACCTCCCGGG CCCCCAAAAA ATTCCAGCTC 100
101 AAGAGCCCTA AAAATCCTTA CCCTGNNAAG GTTTGAGCTT CTCCC 145
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: CaS1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
1 ACGCCGGCCA CAGTTCTTCA GTGAAACGCT TCACTCTCTG GTCATAGAGG 50
51 TAGGAAACTA TAGCTGTCCC AACTAAATGT CAGGACGAAT TAGCCCAGCT 100
101 GGTCACGCTC ACAGTCACCG CCTCCACCAG ACTGAGCGAC CCTCCCAACG 150
151 GGGTTTGCCG TGTGTTGGAGG ACAGCGGAGT TTCGTTGCTG TGTCAATTTG 200
201 TGTAGACGCG GCTGC 215
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: CaS2 primer

```
1 CTGCTCTCTT CTCTTCTTTT CCCCTTTCCT CTCCTCTCCC TTTCCTCAGG 50
51 TCACAGCGGA GTGAATCAGC TCGGTGGTGT CTTTGTCAAC GGGCGGCCAC 100
101 TGCCGGACTC CACCCGGCAG AAGATTGTAG AGCTAGCTCA CAGCGGGGCC 150
151 CGGCCGTGCG ACATTTCCCG AATTCTGCAG GTGATCCTCC CGGCGCCGCC 200
201 CCACTCGCCG CCCCCGCGGC 220
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: CaS4 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
1 GGGCGGCACG GAGGGAGTCA GGAGTGAGCC CGAAGATGGA GAGAAGTCGA 50
51 TTCGCCAGA GAACGCAAGA CCGTGGATCA GAGATGAGTC CCAGGAACCT 100
101 CAGAGAGCGA GGCTGACAGG CCCGGGGAGA GGACCGGGCA GGGACAAACC 150
151 AGCGGACAGA GCAGAGCGCG AAATGGTTGA GACCGGGAAG CGACCT 196
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

1 5'-GTA GGT GGG GAG GAG TTT AGT T-3' 22

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 23  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

1 5'-TCT AAT AAC CAA CCA ACC CCT CC-3

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

1 5'-TTT TTT TGT TTG GAA AGA TAT-3' 21

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 18  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

50 (ii) MOLECULE TYPE: Ms-SNuPE primer from *p16* promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

1 5'-TTT TAG GGG TGT TAT ATT-3' 18

(2) INFORMATION FOR SEQ ID NO:17:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: Ms-SNuPE primer from p16 promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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1 5'-TTT GAG GGA TAG GGT-3' 15

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